

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Kindsvogel, Wayne  
Gross, Jane A.  
Sheppard, Paul
- (ii) TITLE OF INVENTION: Immune Mediators and Related Methods
- (iii) NUMBER OF SEQUENCES: 121
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Townsend and Townsend and Crew LLP  
(B) STREET: Two Embarcadero Center, Eighth Floor  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/261,811  
(B) FILING DATE: 03-MAR-1999  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/480,002  
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/482,133  
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/483,241  
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/005,964  
(B) FILING DATE: 27-OCT-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/657,581  
(B) FILING DATE: 07-JUN-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Parent, Annette S.  
(B) REGISTRATION NUMBER: 42,058  
(C) REFERENCE/DOCKET NUMBER: 014058-005630US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (415) 576-0200  
(B) TELEFAX: (415) 576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGCAAGCTT GAATTCGAGC TCATGGTGTG TCT

33

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGATAT CATGGTGTGT CTGAAGCTCC CTGGAGGCTC CTGCATGACA GCGCTGAC

58

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACTGTCAGC GCTGTCATGC AGGAGCCTCC AGGGAGCTTC AGACACACCA TGATATCG

58

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

B34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTTCTTTAA AAACATCGTG ACTCCGCGTA CACCCCCGCC ATCGGGAGGC GGGTCAGGTG 60

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCACCTG ACCCGCCTCC CGATGGCGGG GGTGTACGCG GAGTCACGAT GTTTTAAAG 60

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTGACACTG ATGGTGCTGA GTCCTCCACT GGCTTTGTCT GACGAAAACC CAGTAGTGC 59

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGTGCACTA CTGGGTTTTC GTCAGACAAA GCCAGTGGGG AGCTCAGCAC CATCAGTGT 59

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA .

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCGGCTGAT GCTCCCCGCT GCACTGT

27

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTCTAGA TCATATAGTT GGAGC

25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAGGGTCTA GATCATAAAG GCCCTGGGTG TCTGGAG

37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGAGGAATTC GCAGAGACCT CCCAGAGACC AGGATCC

37



(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACACTCTAG ATCACTGCAG GAGCCCTGCT GGAGGAG

37

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAGGAATTC TGAGTCCTGG TGACTGCCAT TACCTGT

37

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ.ID NO:14:

GGAGCATCAG CCGGCATCAA AGAAGAACAT

30

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGATGATT AAATGAGTCG CCTCTCGAAG GTGGCTCCAG TGATTAAAGC CAGAATGATG 60  
 GAGTATGGAA CCACAGGAGG TGGAGGCTCT GGAGGTGGAG GCTCAGGAGG A 111

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAGGCTCAG GAGGAGGTGG GTCCGGAGAC TCCGAAAGG 39

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC GATCGTGGAG GATGATTAAA TG 32

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCACCTGAT CCACCCCGCA GGGAGGTGGG 30

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTGGATCAG GTGGCGAAGA CGACATTGAG

30

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGGAATTCT TAACTAGTAG CTGGGGTGAA

30

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGAATTCT TAACTAGTAG CTGGGGTGGA

30

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCACCTGAT CCACCCCGCA GGGAGGTGTG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGCGGGATCC GATCGTGGAG GATGATTAAA TGTTCTTTAA AAACATCGTG ACTCCGCGTA

60

CACCCCGCC AGGAGGTGGA GGCTCTGGAG GTGGAGGCTC AGGAGGA

107

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCGGAATTCT TACTTGCTCC GGGCAGACTC

30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGGCTCAG GAGGAGGTGG GTCTGGCGGT GGAGGTTCCG GCGGAGGCGG TTCAGAAGAC

60

GACATTGAGG CC

72

4-11-84 10:00 AM

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCGGAGGTG GCTCAGGCGG AGGTGGATCT GGAGGTGGAG GCTCACGGCT TGAACAGCCC 60  
 AAT 63

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAGCCTCCA CCTCCAGATC CACCTCCGCC TGAGCCACCT CCGCCAGTCT CTGTCAGCTC 60  
 TGA 63

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCGGAATTCT TAACTAGTCT CTGTCAGCTC TGA 33

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Gly Ala Ser Ala Gly  
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi). SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly. Gly Ser Gly Gly  
1 -5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Gly Gly Ser Gly Gly Ser  
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg  
1 5 10 15

Thr Pro Pro Pro Ser  
20

(2) INFORMATION FOR SEQ ID NO:34:

- (i). SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C). STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Ser Gly Gly Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAGGCTCAG GAGGA

· 15

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met  
1 5 10

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(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: 'SEQ ID NO:40:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe  
1 5 10 15

Lys. Asn Phe Pro  
20

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Pro Gly Gly Ala Ile Ser Asn. Met Tyr Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Arg Leu Glu  
1

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

(2) INFORMATION FOR SEQ ID NO:44:

(ii) MOLECULE TYPE: peptide

(xi). SEQUENCE DESCRIPTION: SEQ ID NO:44:

(2) INFORMATION FOR SEQ ID NO:45:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

(2) INFORMATION FOR SEQ ID NO:46:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Gly Gly Ser Gly Gly Ser Gly  
1 5

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu  
 1                      5                      10                      15  
 Tyr Gly Thr Thr  
                     20

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATCGTGGAG GATGAT

16

## (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAGGATGATT AAATG

15

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu  
 1                      5                      10                      15  
 Tyr Gly Thr Xaa  
                     20

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
 1                      5                      10                      15  
 Gly Thr Xaa

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

Thr Xaa

Xaa

Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Gly	Thr	Xaa
1				5					10					15

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Gly	Thr	Xaa
1				5					10				

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Modified-site  
(B) LOCATION: 13  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(A) NAME/KEY: Modified-site  
(B) LOCATION: 12  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(A) NAME/KEY: Modified-site  
(B) LOCATION: 11  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Lys Ala Arg Met-Met Glu Tyr Gly Thr Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
 1                      5                      10                      15  
 Gly Xaa

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide



## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycine"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
 1                      5                      10                      15  
 Xaa

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosine"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 14
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 13
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

```
/note= "Xaa = argininamide"
```

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Xaa  
1                 5                 10

(D) TOPOLOGY: linear

```
/note= "Xaa = alaninamide"
```

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Xaa  
1 5 10

(D) TOPOLOGY: linear

```
/note= "Xaa = lysinamide"
```

Ser Leu Ser Lys Val Ala Pro Val Ile Xaa  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = isoleucinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ser Leu Ser Lys Val Ala Pro Val Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
 1                      5                      10

"000000" 1000000

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Pro Val Ile Lys Ala Arg Met Met Xaa  
1                      5

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = argininamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Lys Val Ala Pro Val Ile Lys Ala Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = alaninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Lys Val Ala Pro Val Ile Lys Xaa  
1                      5

10004304 033003

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycineamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
 1 5 10 15

Xaa

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosineamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide



## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
 1                      5                      10                      15

10084364 022003

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Leu Ser Lys Val-Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycineamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Xaa  
1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Modified-site  
(B) LOCATION: 14  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosinamide"

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(A) NAME/KEY: Modified-site  
(B) LOCATION: 8  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = lysinamide"

Ser Lys Val Ala Pro Val Ile Xaa  
1 5

(i). SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp  
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATC AAA GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT	48
Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro	
1 5 10 15	
GAC CAA TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC	96
Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe	
20 25 30	
CAT GTG GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT	144
His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe	
35 40 45	
GGA CGA TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT	192
Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala	
50 55 60	
GTG GAC AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG	240
Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met	
65 70 75 80	
ATC	243
Ile	

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro	
1 5 10 15	
Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe	
20 25 30	
His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe	
35 40 45	
Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala	
50 55 60	

Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met  
65 70 75 80

Ile

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAC	GAA	AAC	CCA	GTA	GTG	CAC	TTC	TTT	AAA	AAC	ATC	GTG	ACT	CCG	CGT	48
Asp	Glu	Asn	Pro	Val	Val	His	Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	
1				5					10					15		
ACA	CCC	CCG	CCA	TCG	GGA	GGC	GGG	TCA	GGT	GGA	TCC	GGG	GAC	ACC	CGA	96
Thr	Pro	Pro	Pro	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Asp	Thr	Arg	
			20					25					30			
CCA	CGT	TTC	CTG	TGG	CAG	CCT	AAG	AGG	GAG	TGT	CAT	TTC	TTC	AAT	GGG	144
Pro	Arg	Phe	Leu	Trp	Gln	Pro	Lys	Arg	Glu	Cys	His	Phe	Phe	Asn	Gly	
		35					40					45				
ACG	GAG	CGG	GTG	CGG	TTC	CTG	GAC	AGA	TAC	TTC	TAT	AAC	CAG	GAG	GAG	192
Thr	Glu	Arg	Val	Arg	Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	Asn	Gln	Glu	Glu	
	50					55					60					
TCC	GTG	CGT	TTC	GAC	AGC	GAC	GTG	GGG	GAG	TTC	CGG	GCG	GTG	ACG	GAG	240
Ser	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Phe	Arg	Ala	Val	Thr	Glu	
65					70				75					80		
CTG	GGG	CGG	CCT	GAC	GCT	GAG	TAC	TGG	AAC	AGC	CAG	AAG	GAC	ATC	CTG	288
Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Ile	Leu	
			85						90					95		
GAG	CAG	GCG	CGG	GCC	GCG	GTG	GAC	ACC	TAC	TGC	AGA	CAC	AAC	TAC	GGG	336
Glu	Gln	Ala	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr	Gly	
			100					105					110			
GTT	GTG	GAG	AGC	TTC	ACA	GTG	CAG	CGG	GGA	GCA	TCA	GCC	GGC	ATC	AAA	384
Val	Val	Glu	Ser	Phe	Thr	Val	Gln	Arg	Gly	Ala	Ser	Ala	Gly	Ile	Lys	
		115					120					125				
GAA	GAA	CAT	GTG	ATC	ATC	CAG	GCC	GAG	TTC	TAT	CTG	AAT	CCT	GAC	CAA	432
Glu	Glu	His	Val	Ile	Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	
	130					135					140					

TCA	GGC	GAA	TTT	ATG	TTT	GAC	TTT	GAT	GGT	GAT	GAG	ATT	TTC	CAT	GTG	480
Ser	Gly	Glu	Phe	Met	Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	
145					150					155					160	
GAT	ATG	GCA	AAG	AAG	GAG	ACG	GTC	TGG	CGG	CTT	GAA	GAA	TTT	GGA	CGA	528
Asp	Met	Ala	Lys	Lys	Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	
				165					170						175	
TTT	GCC	AGC	TTT	GAG	GCT	CAA	GGT	GCA	TTG	GCC	AAC	ATA	GCT	GTG	GAC	576
Phe	Ala	Ser	Phe	Glu	Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	
			180					185					190			
AAA	GCC	AAC	CTG	GAA	ATC	ATG	ACA	AAG	CGC	TCC	AAC	TAT	ATG	ATC		621
Lys	Ala	Asn	Leu	Glu	Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Met	Ile		
		195					200					205				

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Asp	Glu	Asn	Pro	Val	Val	His	Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	
1				5					10					15		
Thr	Pro	Pro	Pro	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Asp	Thr	Arg	
			20					25					30			
Pro	Arg	Phe	Leu	Trp	Gln	Pro	Lys	Arg	Glu	Cys	His	Phe	Phe	Asn	Gly	
		35					40					45				
Thr	Glu	Arg	Val	Arg	Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	Asn	Gln	Glu	Glu	
	50					55					60					
Ser	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Phe	Arg	Ala	Val	Thr	Glu	
65					70					75					80	
Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Ile	Leu	
			85						90					95		
Glu	Gln	Ala	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr	Gly	
		100						105					110			
Val	Val	Glu	Ser	Phe	Thr	Val	Gln	Arg	Gly	Ala	Ser	Ala	Gly	Ile	Lys	
		115					120					125				
Glu	Glu	His	Val	Ile	Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	
	130					135					140					
Ser	Gly	Glu	Phe	Met	Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	
145					150					155					160	
Asp	Met	Ala	Lys	Lys	Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	
				165					170						175	

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Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp  
 180 185 190

Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met Ile  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGA	GAC	TCC	GAA	AGG	CAT	TTC	GTG	CAC	CAG	TTC	AAG	GGC	GAG	TGC	TAC	48
Gly	Asp	Ser	Glu	Arg	His	Phe	Val	His	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	
1				5					10					15		
TTC	ACC	AAC	GGG	ACG	CAG	CGC	ATA	CGG	CTC	GTG	ACC	AGA	TAC	ATC	TAC	96
Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Leu	Val	Thr	Arg	Tyr	Ile	Tyr	
			20					25					30			
AAC	CGG	GAG	GAG	TAC	CTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	GAG	TAC	CGC	144
Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	
		35					40					45				
GCG	GTG	ACC	GAG	CTG	GGG	CGG	CAC	TCA	GCC	GAG	TAC	TAC	AAT	AAG	CAG	192
Ala	Val	Thr	Glu	Leu	Gly	Arg	His	Ser	Ala	Glu	Tyr	Tyr	Asn	Lys	Gln	
	50					55				60						
TAC	CTG	GAG	CGA	ACG	CGG	GCC	GAG	CTG	GAC	ACG	GCG	TGC	AGA	CAC	AAC	240
Tyr	Leu	Glu	Arg	Thr	Arg	Ala	Glu	Leu	Asp	Thr	Ala	Cys	Arg	His	Asn	
65				70				75						80		
TAC	GAG	GAG	ACG	GAG	GTC	CCC	ACC	TCC	CTG	CGG						273
Tyr	Glu	Glu	Thr	Glu	Val	Pro	Thr	Ser	Leu	Arg						
				85				90								

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr  
 1 5 10 15  
 Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr  
 20 25 30  
 Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg  
 35 40 45  
 Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln  
 50 55 60  
 Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn  
 65 70 75 80  
 Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..261

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT 48  
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val  
 1 5 10 15  
 TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96  
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
 20 25 30  
 GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG 144  
 Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg  
 35 40 45  
 CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG 192  
 Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu  
 50 55 60  
 CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG 240  
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80



261

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

48

96

GGT	GGG	TCC	GGA	GAC	TCC	GAA	AGG	CAT	TTC	GTG	CAC	CAG	TTC	AAG	GGC	144
Gly	Gly	Ser	Gly	Asp	Ser	Glu	Arg	His	Phe	Val	His	Gln	Phe	Lys	Gly	
		35					40					45				
GAG	TGC	TAC	TTC	ACC	AAC	GGG	ACG	CAG	CGC	ATA	CGG	CTC	GTG	ACC	AGA	192
Glu	Cys	Tyr	Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Leu	Val	Thr	Arg	
	50					55				60						
TAC	ATC	TAC	AAC	CGG	GAG	GAG	TAC	CTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	240
Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	
	65				70					75					80	
GAG	TAC	CGC	GCG	GTG	ACC	GAG	CTG	GGG	CGG	CAC	TCA	GCC	GAG	TAC	TAC	288
Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	His	Ser	Ala	Glu	Tyr	Tyr	
				85				90						95		
AAT	AAG	CAG	TAC	CTG	GAG	CGA	ACG	CGG	GCC	GAG	CTG	GAC	ACG	GCG	TGC	336
Asn	Lys	Gln	Tyr	Leu	Glu	Arg	Thr	Arg	Ala	Glu	Leu	Asp	Thr	Ala	Cys	
			100					105					110			
AGA	CAC	AAC	TAC	GAG	GAG	ACG	GAG	GTC	CCC	ACC	TCC	CTG	CGG	GGT	GGA	384
Arg	His	Asn	Tyr	Glu	Glu	Thr	Glu	Val	Pro	Thr	Ser	Leu	Arg	Gly	Gly	
		115					120					125				
TCA	GGT	GGC	GAA	GAC	GAC	ATT	GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	432
Ser	Gly	Gly	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	
	130					135					140					
ACA	ACT	GTT	TAT	CAG	TCT	CCT	GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	480
Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	
	145				150					155					160	
TTT	GAT	GGT	GAT	GAG	TTG	TTC	TAT	GTG	GAC	TTG	GAT	AAG	AAG	AAA	ACT	528
Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr	
				165				170						175		
GTC	TGG	AGG	CTT	CCT	GAG	TTT	GGC	CAA	TTG	ATA	CTC	TTT	GAG	CCC	CAA	576
Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly	Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln	
			180					185					190			
GGT	GGA	CTG	CAA	AAC	ATA	GCT	GCA	GAA	AAA	CAC	AAC	TTG	GGA	ATC	TTG	624
Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala	Glu	Lys	His	Asn	Leu	Gly	Ile	Leu	
		195				200						205				
ACT	AAG	AGG	TCA	AAT	TTC	ACC	CCA	GCT	ACT							654
Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro	Ala	Thr							
	210					215										

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu  
 1 5 10 15  
 Tyr Gly Thr Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
 20 25 30  
 Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly  
 35 40 45  
 Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg  
 50 55 60  
 Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly  
 65 70 75 80  
 Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr  
 85 90 95  
 Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys  
 100 105 110  
 Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly  
 115 120 125  
 Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly  
 130 135 140  
 Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu  
 145 150 155 160  
 Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr  
 165 170 175  
 Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln  
 180 185 190  
 Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu  
 195 200 205  
 Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr  
 210 215

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

10001204 00000000

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGA	GAC	TCC	GAA	AGG	CAT	TTC	GTG	TTC	CAG	TTC	AAG	GGC	GAG	TGC	TAC	48
Gly	Asp	Ser	Glu	Arg	His	Phe	Val	Phe	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	
1				5					10					15		
TTC	ACC	AAC	GGG	ACG	CAG	CGC	ATA	CGA	TCT	GTG	GAC	AGA	TAC	ATC	TAC	96
Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Ser	Val	Asp	Arg	Tyr	Ile	Tyr	
			20				25						30			
AAC	CGG	GAG	GAG	TAC	CTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	GAG	TAC	CGC	144
Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	
		35					40					45				
GCG	GTG	ACC	GAG	CTG	GGG	CGG	CCA	GAC	CCC	GAG	TAC	TAC	AAT	AAG	CAG	192
Ala	Val	Thr	Glu	Leu	Gly	Arg	Pro	Asp	Pro	Glu	Tyr	Tyr	Asn	Lys	Gln	
	50					55					60					
TAC	CTG	GAG	CAA	ACG	CGG	GCC	GAG	CTG	GAC	ACG	GTG	TGC	AGA	CAC	AAC	240
Tyr	Leu	Glu	Gln	Thr	Arg	Ala	Glu	Leu	Asp	Thr	Val	Cys	Arg	His	Asn	
65					70				75						80	
TAC	GAG	GGG	GTG	GAG	ACC	CAC	ACC	TCC	CTG	CGG						273
Tyr	Glu	Gly	Val	Glu	Thr	His	Thr	Ser	Leu	Arg						
				85					90							

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Gly	Asp	Ser	Glu	Arg	His	Phe	Val	Phe	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	
1				5					10					15		
Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Ser	Val	Asp	Arg	Tyr	Ile	Tyr	
			20					25					30			
Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	
		35					40					45				
Ala	Val	Thr	Glu	Leu	Gly	Arg	Pro	Asp	Pro	Glu	Tyr	Tyr	Asn	Lys	Gln	
	50					55					60					
Tyr	Leu	Glu	Gln	Thr	Arg	Ala	Glu	Leu	Asp	Thr	Val	Cys	Arg	His	Asn	
65					70				75						80	
Tyr	Glu	Gly	Val	Glu	Thr	His	Thr	Ser	Leu	Arg						
				85					90							

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..261

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GAA	GAC	GAC	ATT	GAG	GCC	GAC	CAC	GTA	GGC	GTC	TAT	GGT	ACA	ACT	GTA	48
Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	Gly	Val	Tyr	Gly	Thr	Thr	Val	
1				5					10					15		
TAT	CAG	TCT	CCT	GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	96
Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	
			20					25					30			
GAT	GAG	TGG	TTC	TAT	GTG	GAC	TTG	GAT	AAG	AAG	GAG	ACT	ATC	TGG	ATG	144
Asp	Glu	Trp	Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Glu	Thr	Ile	Trp	Met	
		35					40					45				
CTT	CCT	GAG	TTT	GGC	CAA	TTG	ACA	AGC	TTT	GAC	CCC	CAA	GGT	GGA	CTG	192
Leu	Pro	Glu	Phe	Gly	Gln	Leu	Thr	Ser	Phe	Asp	Pro	Gln	Gly	Gly	Leu	
	50					55					60					
CAA	AAC	ATA	GCT	ACA	GGA	AAA	TAC	ACC	TTG	GGA	ATC	TTG	ACT	AAG	AGG	240
Gln	Asn	Ile	Ala	Thr	Gly	Lys	Tyr	Thr	Leu	Gly	Ile	Leu	Thr	Lys	Arg	
65					70				75					80		
TCA	AAT	TCC	ACC	CCA	GCT	ACT										261
Ser	Asn	Ser	Thr	Pro	Ala	Thr										
					85											

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	Gly	Val	Tyr	Gly	Thr	Thr	Val
1				5					10					15	
Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly
			20				25					30			

Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met  
 35 40 45

Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu  
 50 55 60

Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80

Ser Asn Ser Thr Pro Ala Thr  
 85

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTC	TTT	AAA	AAC	ATC	GTG	ACT	CCG	CGT	ACA	CCC	CCG	CCA	GGA	GGT	GGA	48
Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	Thr	Pro	Pro	Pro	Gly	Gly	Gly	
1				5				10						15		
GGC	TCT	GGA	GGT	GGA	GGC	TCA	GGA	GGA	GGT	GGG	TCC	GGA	GAC	TCC	GAA	96
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Asp	Ser	Glu	
			20					25					30			
AGG	CAT	TTC	GTG	TTC	CAG	TTC	AAG	GGC	GAG	TGC	TAC	TTC	ACC	AAC	GGG	144
Arg	His	Phe	Val	Phe	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Phe	Thr	Asn	Gly	
		35					40					45				
ACG	CAG	CGC	ATA	CGA	TCT	GTG	GAC	AGA	TAC	ATC	TAC	AAC	CGG	GAG	GAG	192
Thr	Gln	Arg	Ile	Arg	Ser	Val	Asp	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	
	50					55					60					
TAC	CTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	GAG	TAC	CGC	GCG	GTG	ACC	GAG	240
Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	
65					70				75					80		
CTG	GGG	CGG	CCA	GAC	CCC	GAG	TAC	TAC	AAT	AAG	CAG	TAC	CTG	GAG	CAA	288
Leu	Gly	Arg	Pro	Asp	Pro	Glu	Tyr	Tyr	Asn	Lys	Gln	Tyr	Leu	Glu	Gln	
			85					90						95		
ACG	CGG	GCC	GAG	CTG	GAC	ACG	GTG	TGC	AGA	CAC	AAC	TAC	GAG	GGG	GTG	336
Thr	Arg	Ala	Glu	Leu	Asp	Thr	Val	Cys	Arg	His	Asn	Tyr	Glu	Gly	Val	
			100					105						110		

GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT	384
Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile	
115 120 125	
GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT	432
Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro	
130 135 140	
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC	480
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe	
145 150 155 160	
TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT	528
Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe	
165 170 175	
GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT	576
Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala	
180 185 190	
ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC	624
Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr	
195 200 205	
CCA GCT ACT	633
Pro Ala Thr	
210	

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	Thr	Pro	Pro	Pro	Gly	Gly	Gly	1	5	10	15
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Asp	Ser	Glu	20	25	30	
Arg	His	Phe	Val	Phe	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Phe	Thr	Asn	Gly	35	40	45	
Thr	Gln	Arg	Ile	Arg	Ser	Val	Asp	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	50	55	60	
Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	65	70	75	80
Leu	Gly	Arg	Pro	Asp	Pro	Glu	Tyr	Tyr	Asn	Lys	Gln	Tyr	Leu	Glu	Gln	85	90	95	
Thr	Arg	Ala	Glu	Leu	Asp	Thr	Val	Cys	Arg	His	Asn	Tyr	Glu	Gly	Val	100	105	110	

Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile  
 115 120 125  
 Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro  
 130 135 140  
 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe  
 145 150 155 160  
 Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe  
 165 170 175  
 Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala  
 180 185 190  
 Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr  
 195 200 205  
 Pro Ala Thr  
 210

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..312

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC AGG ACA GAG GCC	48
Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala	
1 5 10 15	
CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA GAT TTC TAC CCA	96
Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro	
20 25 30	
GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG GAG GAG ACA GTG	144
Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val	
35 40 45	
GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG	192
Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln	
50 55 60	
GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA GAG GTC TAC ACC	240
Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr	
65 70 75 80	

10001301 033003



TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG 288  
 Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp  
                     85                    90                    95

AGG GCA CAG TCC GAG TCT GCC CGG 312  
 Arg Ala Gln Ser Glu Ser Ala Arg  
                     100

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala  
   1                    5                    10                    15  
 Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro  
                     20                    25                    30  
 Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val  
                     35                    40                    45  
 Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln  
                     50                    55                    60  
 Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr  
   65                    70                    75                    80  
 Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp  
                     85                    90                    95  
 Arg Ala Gln Ser Glu Ser Ala Arg  
                     100

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 588 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..588

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT	48
Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val	
1 5 10 15	
TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT	96
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	
GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG	144
Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg	
35 40 45	
CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu	
50 55 60	
CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	
TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC	288
Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe	
85 90 95	
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT	336
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe	
100 105 110	
GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT	384
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn	
115 120 125	
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC	432
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn	
130 135 140	
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT	480
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser	
145 150 155 160	
GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG	528
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu	
165 170 175	
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG	576
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu	
180 185 190	
CTG ACA GAG ACT	588
Leu Thr Glu Thr	
195	

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val  
1 5 10 15  
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
20 25 30  
Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg  
35 40 45  
Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu  
50 55 60  
Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg  
65 70 75 80  
Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe  
85 90 95  
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe  
100 105 110  
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn  
115 120 125  
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn  
130 135 140  
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser  
145 150 155 160  
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu  
165 170 175  
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu  
180 185 190  
Leu Thr Glu Thr  
195

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1344

AGT Ser 1	CGC Arg	CTC Leu	TCG Ser	AAG Lys 5	GTG Val	GCT Ala	CCA Pro	GTG Val	ATT Ile 10	AAA Lys	GCC Ala	AGA Arg	ATG Met	ATG Met 15	GAG Glu	48
TAT Tyr	GGA Gly	ACC Thr	ACA Thr 20	GGA Gly	GGT Gly	GGA Gly	GGC Gly	TCT Ser 25	GGA Gly	GGT Gly	GGA Gly	GGC Gly	TCA Ser 30	GGA Gly	GGA Gly	96
GGT Gly	GGG Gly	TCC Ser 35	GGA Gly	GAC Asp	TCC Ser	GAA Glu	AGG Arg 40	CAT His	TTC Phe	GTG Val	CAC His	CAG Gln 45	TTC Phe	AAG Lys	GGC Gly	144
GAG Glu	TGC Cys 50	TAC Tyr	TTC Phe	ACC Thr	AAC Asn	GGG Gly 55	ACG Thr	CAG Gln	CGC Arg	ATA Ile	CGG Arg 60	CTC Leu	GTG Val	ACC Thr	AGA Arg	192
TAC Tyr 65	ATC Ile	TAC Tyr	AAC Asn	CGG Arg	GAG Glu 70	GAG Glu	TAC Tyr	CTG Leu	CGC Arg	TTC Phe 75	GAC Asp	AGC Ser	GAC Asp	GTG Val	GGC Gly 80	240
GAG Glu	TAC Tyr	CGC Arg	GCG Ala	GTG Val 85	ACC Thr	GAG Glu	CTG Leu	GGG Gly	CGG Arg 90	CAC His	TCA Ser	GCC Ala	GAG Glu	TAC Tyr 95	TAC Tyr	288
AAT Asn	AAG Lys	CAG Gln	TAC Tyr 100	CTG Leu	GAG Glu	CGA Arg	ACG Thr	CGG Arg 105	GCC Ala	GAG Glu	CTG Leu	GAC Asp	ACG Thr 110	GCG Ala	TGC Cys	336
AGA Arg	CAC His	AAC Asn 115	TAC Tyr	GAG Glu	GAG Glu	ACG Thr	GAG Glu 120	GTC Val	CCC Pro	ACC Thr	TCC Ser	CTG Leu 125	CGG Arg	GGT Gly	GGA Gly	384
TCA Ser	GGT Gly 130	GGC Gly	GAA Glu	GAC Asp	GAC Asp	ATT Ile 135	GAG Glu	GCC Ala	GAC Asp	CAC His	GTA Val 140	GGC Gly	TTC Phe	TAT Tyr	GGT Gly	432
ACA Thr 145	ACT Thr	GTT Val	TAT Tyr	CAG Gln	TCT Ser 150	CCT Pro	GGA Gly	GAC Asp	ATT Ile	GGC Gly 155	CAG Gln	TAC Tyr	ACA Thr	CAT His	GAA Glu 160	480
TTT Phe	GAT Asp	GGT Gly	GAT Asp	GAG Glu 165	TTG Leu	TTC Phe	TAT Tyr	GTG Val	GAC Asp 170	TTG Leu	GAT Asp	AAG Lys	AAG Lys	AAA Lys 175	ACT Thr	528
GTC Val	TGG Trp	AGG Arg	CTT Leu 180	CCT Pro	GAG Glu	TTT Phe	GGC Gly	CAA Gln 185	TTG Leu	ATA Ile	CTC Leu	TTT Phe 190	GAG Glu	CCC Pro	CAA Gln	576
GGT Gly	GGA Gly	CTG Leu 195	CAA Gln	AAC Asn	ATA Ile	GCT Ala	GCA Ala 200	GAA Glu	AAA Lys	CAC His	AAC Asn	TTG Leu 205	GGA Gly	ATC Ile	TTG Leu	624
ACT Thr	AAG Lys 210	AGG Arg	TCA Ser	AAT Asn	TTC Phe	ACC Thr 215	CCA Pro	GCT Ala	ACC Thr	AAT Asn	GAG Glu 220	GCT Ala	CCT Pro	CAA Gln	GCG Ala	672
ACT Thr 225	GTG Val	TTC Phe	CCC Pro	AAG Lys	TCC Ser 230	CCT Pro	GTG Val	CTG Leu	CTG Leu	GGT Gly 235	CAG Gln	CCC Pro	AAC Asn	ACC Thr	CTT Leu 240	720

ATC	TGC	TTT	GTG	GAC	AAC	ATC	TTC	CCA	CCT	GTG	ATC	AAC	ATC	ACA	TGG	768
Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	
				245					250					255		
CTC	AGA	AAT	AGC	AAG	TCA	GTC	ACA	GAC	GGC	GTT	TAT	GAG	ACC	AGC	TTC	816
Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	
			260					265					270			
CTC	GTC	AAC	CGT	GAC	CAT	TCC	TTC	CAC	AAG	CTG	TCT	TAT	CTC	ACC	TTC	864
Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	
		275					280					285				
ATC	CCT	TCT	GAT	GAT	GAC	ATT	TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC	912
Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	
	290					295					300					
CTG	GAG	GAG	CCG	GTT	CTG	AAA	CAC	TGG	GAA	CCT	GAG	ATT	CCA	GCC	CCC	960
Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	
305					310				315						320	
ATG	TCA	GAG	CTG	ACA	GAG	ACT	GGC	GGA	GGT	GGC	TCA	GGC	GGA	GGT	GGA	1008
Met	Ser	Glu	Leu	Thr	Glu	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				325				330					335			
TCT	GGA	GGT	GGA	GGC	TCA	CGG	CTT	GAA	CAG	CCC	AAT	GTC	GCC	ATC	TCC	1056
Ser	Gly	Gly	Gly	Gly	Ser	Arg	Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	
			340					345					350			
CTG	TCC	AGG	ACA	GAG	GCC	CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGT	TCG	1104
Leu	Ser	Arg	Thr	Glu	Ala	Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	
		355					360					365				
GTG	ACA	GAT	TTC	TAC	CCA	GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	AGG	AAT	1152
Val	Thr	Asp	Phe	Tyr	Pro	Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	
	370					375					380					
GGC	CAG	GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	1200
Gly	Gln	Glu	Glu	Thr	Val	Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	
385					390					395					400	
GGG	GAC	TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	1248
Gly	Asp	Trp	Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	
				405					410					415		
CAG	GGA	GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	1296
Gln	Gly	Glu	Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	
			420					425					430			
CCC	ATC	ACT	GTG	GAG	TGG	AGG	GCA	CAG	TCC	GAG	TCT	GCC	CGG	AGC	AAG	1344
Pro	Ile	Thr	Val	Glu	Trp	Arg	Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys	
		435					440					445				

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

[illegible]

Ser	Arg	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Glu	
1				5					10					15	
Tyr	Gly	Thr	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			20					25					30		
Gly	Gly	Ser	Gly	Asp	Ser	Glu	Arg	His	Phe	Val	His	Gln	Phe	Lys	Gly
		35					40					45			
Glu	Cys	Tyr	Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Leu	Val	Thr	Arg
	50					55					60				
Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly
65					70					75					80
Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	His	Ser	Ala	Glu	Tyr	Tyr
				85					90					95	
Asn	Lys	Gln	Tyr	Leu	Glu	Arg	Thr	Arg	Ala	Glu	Leu	Asp	Thr	Ala	Cys
			100					105					110		
Arg	His	Asn	Tyr	Glu	Glu	Thr	Glu	Val	Pro	Thr	Ser	Leu	Arg	Gly	Gly
		115					120					125			
Ser	Gly	Gly	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly
	130					135					140				
Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu
145					150					155					160
Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr
				165					170					175	
Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly	Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln
			180					185					190		
Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala	Glu	Lys	His	Asn	Leu	Gly	Ile	Leu
		195					200					205			
Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro	Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala
	210					215					220				
Thr	Val	Phe	Pro	Lys	Ser	Pro	Val	Leu	Leu	Gly	Gln	Pro	Asn	Thr	Leu
225					230					235					240
Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp
				245					250					255	
Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe
			260					265					270		
Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe
		275					280					285			
Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly
	290					295					300				
Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro
305					310					315					320

Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 325 330 335

Ser Gly Gly Gly Gly Ser Arg Leu Glu Gln Pro Asn Val Ala Ile Ser  
 340 345 350

Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser  
 355 360 365

Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn  
 370 375 380

Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn  
 385 390 395 400

Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His  
 405 410 415

Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser  
 420 425 430

Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys  
 435 440 445

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CGG CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC	48
Arg Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala	
1 5 10 15	
CTC AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA	96
Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro	
20 25 30	
GCC AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG	144
Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val	
35 40 45	
GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG	192
Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln	
50 55 60	

10001361 033003

GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CGG	CGG	GGA	GAG	GTC	TAC	ACC	240
Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	Arg	Arg	Gly	Glu	Val	Tyr	Thr	
65					70					75					80	
TGC	CAC	GTG	GAG	CAT	CCG	AGC	CTG	AAG	AGC	CCC	ATC	ACT	GTG	GAG	TGG	288
Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr	Val	Glu	Trp	
			85						90					95		
AGG	GCA	CAG	TCT	GAG	TCT	GCC	CGG	AGC	AAG							318
Arg	Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys							
			100						105							

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg	Leu	Glu	Gln	Pro	Asn	Val	Val	Ile	Ser	Leu	Ser	Arg	Thr	Glu	Ala	
1				5					10					15		
Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr	Asp	Phe	Tyr	Pro	
			20					25					30			
Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln	Glu	Glu	Thr	Val	
		35				40						45				
Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp	Trp	Thr	Phe	Gln	
	50					55					60					
Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	Arg	Arg	Gly	Glu	Val	Tyr	Thr	
65					70					75					80	
Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr	Val	Glu	Trp	
				85					90					95		
Arg	Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys							
			100						105							

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1323



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTC	TTT	AAA	AAC	ATC	GTG	ACT	CCG	CGT	ACA	CCC	CCG	CCA	GGA	GGT	GGA	48
Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	Thr	Pro	Pro	Pro	Gly	Gly	Gly	
1				5					10					15		
GGC	TCT	GGA	GGT	GGA	GGC	TCA	GGA	GGA	GGT	GGG	TCC	GGA	GAC	TCC	GAA	96
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Asp	Ser	Glu	
			20					25					30			
AGG	CAT	TTC	GTG	TTC	CAG	TTC	AAG	GGC	GAG	TGC	TAC	TTC	ACC	AAC	GGG	144
Arg	His	Phe	Val	Phe	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Phe	Thr	Asn	Gly	
		35					40					45				
ACG	CAG	CGC	ATA	CGA	TCT	GTG	GAC	AGA	TAC	ATC	TAC	AAC	CGG	GAG	GAG	192
Thr	Gln	Arg	Ile	Arg	Ser	Val	Asp	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	
	50					55					60					
TAC	CTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	GAG	TAC	CGC	GCG	GTG	ACC	GAG	240
Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	
65					70				75						80	
CTG	GGG	CGG	CCA	GAC	CCC	GAG	TAC	TAC	AAT	AAG	CAG	TAC	CTG	GAG	CAA	288
Leu	Gly	Arg	Pro	Asp	Pro	Glu	Tyr	Tyr	Asn	Lys	Gln	Tyr	Leu	Glu	Gln	
				85					90					95		
ACG	CGG	GCC	GAG	CTG	GAC	ACG	GTG	TGC	AGA	CAC	AAC	TAC	GAG	GGG	GTG	336
Thr	Arg	Ala	Glu	Leu	Asp	Thr	Val	Cys	Arg	His	Asn	Tyr	Glu	Gly	Val	
			100					105					110			
GAG	ACC	CAC	ACC	TCC	CTG	CGG	GGT	GGA	TCA	GGT	GGC	GAA	GAC	GAC	ATT	384
Glu	Thr	His	Thr	Ser	Leu	Arg	Gly	Gly	Ser	Gly	Gly	Glu	Asp	Asp	Ile	
		115					120					125				
GAG	GCC	GAC	CAC	GTA	GGC	GTC	TAT	GGT	ACA	ACT	GTA	TAT	CAG	TCT	CCT	432
Glu	Ala	Asp	His	Val	Gly	Val	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro	
	130					135					140					
GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	GAT	GAG	TGG	TTC	480
Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Trp	Phe	
145				150				155							160	
TAT	GTG	GAC	TTG	GAT	AAG	AAG	GAG	ACT	ATC	TGG	ATG	CTT	CCT	GAG	TTT	528
Tyr	Val	Asp	Leu	Asp	Lys	Lys	Glu	Thr	Ile	Trp	Met	Leu	Pro	Glu	Phe	
			165					170						175		
GGC	CAA	TTG	ACA	AGC	TTT	GAC	CCC	CAA	GGT	GGA	CTG	CAA	AAC	ATA	GCT	576
Gly	Gln	Leu	Thr	Ser	Phe	Asp	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	Ala	
			180					185					190			
ACA	GGA	AAA	TAC	ACC	TTG	GGA	ATC	TTG	ACT	AAG	AGG	TCA	AAT	TCC	ACC	624
Thr	Gly	Lys	Tyr	Thr	Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Ser	Thr	
		195					200					205				
CCA	GCT	ACC	AAT	GAG	GCT	CCT	CAA	GCG	ACT	GTG	TTC	CCC	AAG	TCC	CCT	672
Pro	Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	Pro	
	210					215					220					
GTG	CTG	CTG	GGT	CAG	CCC	AAA	ACC	CTT	ATC	TGC	TTT	GTG	GAC	AAC	ATC	720
Val	Leu	Leu	Gly	Gln	Pro	Lys	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile	
225				230						235					240	

10001201 023002

TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC 768  
 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val  
 245 250 255

ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC 816  
 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser  
 260 265 270

TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT 864  
 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile  
 275 280 285

TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA 912  
 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys  
 290 295 300

CAT TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT 960  
 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr  
 305 310 315 320

GGC GGA GGT GGC TCA GGC GGA GGT GGA TCT GGA GGT GGA GGC TCA CGG 1008  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg  
 325 330 335

CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC CTC 1056  
 Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu  
 340 345 350

AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA GCC 1104  
 Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala  
 355 360 365

AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG GGG 1152  
 Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly  
 370 375 380

GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG GTC 1200  
 Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val  
 385 390 395 400

CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC TGC 1248  
 Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys  
 405 410 415

CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG AGG 1296  
 His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg  
 420 425 430

GCA CAG TCT GAG TCT GCC CGG AGC AAG 1323  
 Ala Gln Ser Glu Ser Ala Arg Ser Lys  
 435 440

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly  
 1 5 10 15  
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Asp Ser Glu  
 20 25 30  
 Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly  
 35 40 45  
 Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu  
 50 55 60  
 Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu  
 65 70 75 80  
 Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln  
 85 90 95  
 Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val  
 100 105 110  
 Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile  
 115 120 125  
 Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro  
 130 135 140  
 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe  
 145 150 155 160  
 Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe  
 165 170 175  
 Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala  
 180 185 190  
 Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr  
 195 200 205  
 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro  
 210 215 220  
 Val Leu Leu Gly Gln Pro Lys Thr Leu Ile Cys Phe Val Asp Asn Ile  
 225 230 235 240  
 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val  
 245 250 255  
 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser  
 260 265 270  
 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile  
 275 280 285  
 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys  
 290 295 300  
 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr  
 305 310 315 320

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg  
 325 330 335

Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu  
 340 345 350

Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala  
 355 360 365

Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly  
 370 375 380

Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val  
 385 390 395 400

Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys  
 405 410 415

His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg  
 420 425 430

Ala Gln Ser Glu Ser Ala Arg Ser Lys  
 435 440

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAA	GAC	GAC	ATT	GAG	GCC	GAC	CAC	GTA	GGC	GTC	TAT	GGT	ACA	ACT	GTA	48
Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	Gly	Val	Tyr	Gly	Thr	Thr	Val	
1				5				10					15			
TAT	CAG	TCT	CCT	GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	96
Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	
			20					25					30			
GAT	GAG	TGG	TTC	TAT	GTG	GAC	TTG	GAT	AAG	AAG	GAG	ACT	ATC	TGG	ATG	144
Asp	Glu	Trp	Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Glu	Thr	Ile	Trp	Met	
		35					40				45					
CTT	CCT	GAG	TTT	GGC	CAA	TTG	ACA	AGC	TTT	GAC	CCC	CAA	GGT	GGA	CTG	192
Leu	Pro	Glu	Phe	Gly	Gln	Leu	Thr	Ser	Phe	Asp	Pro	Gln	Gly	Gly	Leu	
		50				55					60					

CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	
TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC	288
Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe	
85 90 95	
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT	336
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe	
100 105 110	
GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT	384
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn	
115 120 125	
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC	432
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn	
130 135 140	
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT	480
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser	
145 150 155 160	
GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG	528
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu	
165 170 175	
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG	576
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu	
180 185 190	
CTG ACA GAG ACT	588
Leu Thr Glu Thr	
195	

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val	
1 5 10 15	
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met	
35 40 45	
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu	
50 55 60	

Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80  
 Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe  
 85 90 95  
 Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe  
 100 105 110  
 Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn  
 115 120 125  
 Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn  
 130 135 140  
 Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser  
 145 150 155 160  
 Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu  
 165 170 175  
 Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu  
 180 185 190  
 Leu Thr Glu Thr  
 195

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..702

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA	48
Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly	
1 5 10 15	
GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCT GGC GGT GGA GGT	96
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
20 25 30	
TCC GGC GGA GGC GGT TCA GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC	144
Ser Gly Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly	
35 40 45	
GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC	192
Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr	
50 55 60	

ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG 240  
 Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys  
 65 70 75 80  
 AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT 288  
 Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe  
 85 90 95  
 GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG 336  
 Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu  
 100 105 110  
 GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT 384  
 Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala  
 115 120 125  
 CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC 432  
 Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro  
 130 135 140  
 AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC 480  
 Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn  
 145 150 155 160  
 ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG 528  
 Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu  
 165 170 175  
 ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT 576  
 Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr  
 180 185 190  
 CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG 624  
 Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu  
 195 200 205  
 CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT 672  
 His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile  
 210 215 220  
 CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT 702  
 Pro Ala Pro Met Ser Glu Leu Thr Glu Thr  
 225 230

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly  
 1 5 10 15

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 20 25 30  
 Ser Gly Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly  
 35 40 45  
 Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr  
 50 55 60  
 Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys  
 65 70 75 80  
 Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe  
 85 90 95  
 Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu  
 100 105 110  
 Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala  
 115 120 125  
 Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro  
 130 135 140  
 Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn  
 145 150 155 160  
 Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu  
 165 170 175  
 Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr  
 180 185 190  
 Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu  
 195 200 205  
 His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile  
 210 215 220  
 Pro Ala Pro Met Ser Glu Leu Thr Glu Thr  
 225 230

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..279



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGG GAC ACC CGA CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT 48  
 Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His  
 1 5 10 15

TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT 96  
 Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr  
 20 25 30

AAC CAG GAG GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG 144  
 Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg  
 35 40 45

GCG GTG ACG GAG CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG 192  
 Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln  
 50 55 60

AAG GAC ATC CTG GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA 240  
 Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg  
 65 70 75 80

CAC AAC TAC GGG GTT GTG GAG AGC TTC ACA GTG CAG CGG 279  
 His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

B3  
 Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His  
 1 5 10 15

Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr  
 20 25 30

Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg  
 35 40 45

Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln  
 50 55 60

Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg  
 65 70 75 80

His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg  
 85 90

[illegible]

10081281 1320002

(1) GENERAL INFORMATION:

(i) APPLICANT: ZymoGenetics, Inc.  
1201 Eastlake Avenue East  
Seattle  
WA  
USA  
98102

Anergen, Inc.  
301 Penobscot Drive  
Redwood City  
CA  
USA  
94063

(ii) TITLE OF INVENTION: IMMUNE MEDIATORS AND RELATED METHODS

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: ZymoGenetics, Inc.  
(B) STREET: 1201 Eastlake Avenue East  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/480,002  
(B) FILING DATE: 07-JUN-1995

Anergen, Inc.  
301 Penobscot Drive  
Redwood City  
CA  
USA  
94063

(iii) NUMBER OF SEQUENCES: 61

(A) ADDRESSEE: ZymoGenetics, Inc.  
(B) STREET: 1201 Eastlake Avenue East  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98102

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: US 08/480,002  
(B) FILING DATE: 07-JUN-1995

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/483,241
- (B) FILING DATE: 07-JUN-1995

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/482,133
- (B) FILING DATE: 07-JUN-1995

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/005,964
- (B) FILING DATE: 27-OCT-1995

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Parker, Gary E
- (B) REGISTRATION NUMBER: 31-648

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206-442-6673
- (B) TELEFAX: 206-442-6678

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGCAAGCTT GAATTCGAGC TCATGGTGTG TCT

33

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Sub  
B34

2000-10-13 13:44:00



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGATAT CATGGTGTGT CTGAAGCTCC CTGGAGGCTC CTGCATGACA GCGCTGAC

58

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACTGTCAGC GCTGTCATGC AGGAGCCTCC AGGGAGCTTC AGACACACCA TGATATCG

58

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTTCTTTAA AAACATCGTG ACTCCGCGTA CACCCCCGCC ATCGGGAGGC GGGTCAGGTG

60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCACCTG ACCCGCCTCC CGATGGCGGG GGTGTACGCG GAGTCACGAT GTTTTAAAG 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTGACACTG ATGGTGCTGA GCTCCCCACT GGCTTTGTCT GACGAAAACC CAGTAGTGC 59

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGTGACTA CTGGGTTTTC GTCAGACAAA GCCAGTGGGG AGCTCAGCAC CATCAGTGT 59

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCGGCTGAT GCTCCCCGCT GCACTGT

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTCTAGA TCATATAGTT GGAGC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAGGGTCTA GATCATAAAG GCCCTGGGTG TCTGGAG

37

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGAGGAATTC GCAGAGACCT CCCAGAGACC AGGATCC

37

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACACTCTAG ATCACTGCAG GAGCCCTGCT GGAGGAG

37

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CGAGGAATTC GCAGAGACCT CCCAGAGACC AGGATCC



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAGGAATTC TGAGTCCTGG TGACTGCCAT TACCTGT

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGCATCAG CCGGCATCAA AGAAGAACAT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGATGATT AAATGAGTCG CCTCTCGAAG GTGGCTCCAG TGATTAAAGC CAGAATGATG

60

GAGTATGGAA CCACAGGAGG TGGAGGCTCT GGAGGTGGAG GCTCAGGAGG A

111

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAGGCTCAG GAGGAGGTGG GTCCGGAGAC TCCGAAAGG

39

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC GATCGTGGAG GATGATTAAA TG

32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCACCTGAT CCACCCGCA GGGAGGTGGG

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: cDNA

GGTGGATCAG GTGGCGAAGA CGACATTGAG

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGGAATTCT TAACTAGTAG CTGGGGTGAA

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGAATTCT TAACTAGTAG CTGGGGTGGG

30

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCACCTGAT CCACCCGCA GGGAGGTGTG

30

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGCGGGATCC GATCGTGGAG GATGATTAAA TGTTCTTTAA AAACATCGTG ACTCCGCGTA

60

CACCCCGCC AGGAGGTGGA GGCTCTGGAG GTGGAGGCTC AGGAGGA

107

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

103-23-102202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCGGAATTCT TACTTGCTCC GGGCAGACTC

30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGGCTCAG GAGGAGGTGG GTCTGGCGGT GGAGGTTCCG GCGGAGGCGG TTCAGAAGAC

60

GACATTGAGG CC

72

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCGGAGGTG GCTCAGGCGG AGGTGGATCT GGAGGTGGAG GCTCACGGCT TGAACAGCCC

60

AAT

63

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAGCCTCCA CCTCCAGATC CACCTCCGCC TGAGCCACCT CCGCCAGTCT CTGTCAGCTC 60  
TGA 63

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCGGAATTCT TAACTAGTCT CTGTCAGCTC TGA 33

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Ala Ser Ala Gly

1

5

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Gly Ser Gly Gly  
1 5

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Gly Gly Ser Gly Gly Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 20 25

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg  
 1 5 10 15

Thr Pro Pro Pro Ser  
 20

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5



## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAGGCTCAG GAGGA  
15

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

10004304-000000

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe  
1                      5                      10                      15

Lys Met Phe Pro  
                    20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

2004-06-04 10:00:00

(B) LOCATION: 1..654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG	48
Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu	
1 5 10 15	
TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA	96
Tyr Gly Thr Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
20 25 30	
GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC	144
Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly	
35 40 45	
GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA	192
Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg	
50 55 60	
TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC	240
Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly	
65 70 75 80	
GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC	288
Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr	
85 90 95	
AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC	336
Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys	
100 105 110	
AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA	384
Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly	
115 120 125	
TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT	432
Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly	
130 135 140	
ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA	480
Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu	
145 150 155 160	

TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT 528  
 Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr  
                   165                  170                  175

GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA 576  
 Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln  
                   180                  185                  190

GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG 624  
 Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu  
                   195                  200                  205

ACT AAG AGG TCA AAT TTC ACC CCA GCT ACT 654  
 Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr  
                   210                  215

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC GAG TGC TAC 48  
 Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr  
   1                  5                  10                  15

TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA TAC ATC TAC 96  
 Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr  
                   20                  25                  30

AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC 144  
 Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg  
                   35                  40                  45

CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG 192  
Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu  
50 55 60

CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG 240  
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80

TCA AAT TTC ACC CCA GCT ACT 261  
 Ser Asn Phe Thr Pro Ala Thr  
 85

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs.
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA 48  
 Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly  
 1 5 10 15

GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA 96  
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu  
 20 25 30

AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG 144  
 Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly  
 35 40 45

ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG 192  
 Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu  
 50 55 60

TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG 240  
 Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu  
 65 70 75 80

CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA 288  
 Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln  
 85 90 95

ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG 336  
 Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val  
 100 105 110

GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT 384  
 Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile  
 115 120 125

GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT 432  
 Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro  
 130 135 140

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC 480  
 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe  
 145 150 155 160

TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT 528  
 Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe  
 165 170 175

GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT 576  
 Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala  
 180 185 190

ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC 624  
 Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr  
 195 200 205

CCA GCT ACT 633  
 Pro Ala Thr  
 210

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGA GAC TCC GAA AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC	48
Gly Asp Ser Glu Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr	
1 5 10 15	
TTC ACC AAC GGG ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC	96
Phe Thr Asn Gly Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr	
20 25 30	
AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC	144
Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg	
35 40 45	
GCG GTG ACC GAG CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG	192
Ala Val Thr Glu Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln	
50 55 60	
TAC CTG GAG CAA ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC	240
Tyr Leu Glu Gln Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn	
65 70 75 80	
TAC GAG GGG GTG GAG ACC CAC ACC TCC CTG CGG	273
Tyr Glu Gly Val Glu Thr His Thr Ser Leu Arg	
85 90	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid

(D) TOPOLOGY: linear.

(ix) FEATURE:

(B) LOCATION: 1..261

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA 48  
Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val  
1 5 10 15

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96  
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
20 25 30

GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG 144  
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met  
35 40 45

CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG 192  
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu  
50 55 60

CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG 240  
Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg  
65 70 75 80

TCA AAT TCC ACC CCA GCT ACT  
Ser Asn Ser Thr Pro Ala Thr  
85

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATCGTGGAG GATGAT

16

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAC GAA AAC CCA GTA GTG CAC TTC TTT AAA AAC ATC GTG ACT CCG CGT	48
Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg	
1 5 10 15	
ACA CCC CCG CCA TCG GGA GGC GGG TCA GGT GGA TCC GGG GAC ACC CGA	96
Thr Pro Pro Pro Ser Gly Gly Gly Ser Gly Gly Ser Gly Asp Thr Arg	
20 25 30	
CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT TTC TTC AAT GGG	144
Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly	
35 40 45	
ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT AAC CAG GAG GAG	192
Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu	
50 55 60	
TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG	240
Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu	

65	70	75	80	
CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG AAG GAC ATC CTG				288
Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu				
	85	90	95	
GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA CAC AAC TAC GGG				336
Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly				
	100	105	110	
GTT GTG GAG AGC TTC ACA GTG CAG CGG GGA GCA TCA GCC GGC ATC AAA				384
Val Val Glu Ser Phe Thr Val Gln Arg Gly Ala Ser Ala Gly Ile Lys				
	115	120	125	
GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT GAC CAA				432
Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln				
	130	135	140	
TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC CAT GTG				480
Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val				
	145	150	155	160
GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT GGA CGA				528
Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg				
	165	170	175	
TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT GTG GAC				576
Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp				
	180	185	190	
AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG ATC				621
Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met Ile				
	195	200	205	

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..279

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGG GAC ACC CGA CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT 48  
 Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His  
 1 5 10 15

TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT 96  
 Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr  
 20 25 30

AAC CAG GAG GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG 144  
 Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg  
 35 40 45

GCG GTG ACG GAG CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG 192  
 Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln  
 50 55 60

AAG GAC ATC CTG GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA 240  
 Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg  
 65 70 75 80

CAC AAC TAC GGG GTT GTG GAG AGC TTC ACA GTG CAG CGG 279  
 His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATC AAA GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT	48
Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro	
1 5 10 15	
GAC CAA TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC	96
Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe	
20 25 30	
CAT GTG GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT	144
His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe	
35 40 45	
GGA CGA TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT	192
Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala	
50 55 60	
GTG GAC AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG	240
Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met	
65 70 75 80	
ATC	243
Ile	

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 702 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..702

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA	48
Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly	
1 5 10 15	
GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCT GGC GGT GGA GGT	96
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
20 25 30	
TCC GGC GGA GGC GGT TCA GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC	144
Ser Gly Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly	
35 40 45	
GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC	192
Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr	
50 55 60	
ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG	240
Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys	
65 70 75 80	
AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT	288
Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe	
85 90 95	
GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG	336
Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu	
100 105 110	
GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT	384
Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala	
115 120 125	
CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC	432
Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro	
130 135 140	
AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC	480
Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn	
145 150 155 160	
ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG	528

Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu  
 165 170 175

ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT 576  
 Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr  
 180 185 190

CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG 624  
 Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu  
 195 200 205

CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT 672  
 His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile  
 210 215 220

CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT 702  
 Pro Ala Pro Met Ser Glu Leu Thr Glu Thr  
 225 230

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA 48  
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val  
 1 5 10 15

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96  
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
 20 25 30



GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met 35 40 45	144
CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu 50 55 60	192
CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg 65 70 75 80	240
TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe 85 90 95	288
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe 100 105 110	336
GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn 115 120 125	384
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn 130 135 140	432
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser 145 150 155 160	480
GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu 165 170 175	528
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu 180 185 190	576
CTG ACA GAG ACT Leu Thr Glu Thr 195	588

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1323

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA 48  
 Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly  
 1 5 10 15  
 GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA 96  
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu  
 20 25 30  
 AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG 144  
 Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly  
 35 40 45  
 ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG 192  
 Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu  
 50 55 60  
 TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG 240  
 Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu  
 65 70 75 80  
 CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA 288  
 Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln  
 85 90 95  
 ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG 336  
 Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val

100	105	110	
GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT			384
Glu Thr His Thr Ser Leu Arg Gly-Gly Ser Gly Gly Glu Asp Asp Ile			
115	120	125	
GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT			432
Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro			
130	135	140	
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC			480
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe			
145	150	155	160
TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT			528
Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe			
165	170	175	
GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT			576
Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala			
180	185	190	
ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC			624
Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr			
195	200	205	
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT			672
Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro			
210	215	220	
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC			720
Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile			
225	230	235	240
TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC			768
Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val			
245	250	255	
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC			816
Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser			
260	265	270	
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT			864
Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile			
275	280	285	

TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA	912
Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys	
290 295 300	
CAT TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT	960
His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr	
305 310 315 320	
GGC GGA GGT GGC TCA GGC GGA GGT GGA TCT GGA GGT GGA GGC TCA CGG	1008
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg	
325 330 335	
CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC CTC	1056
Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu	
340 345 350	
AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA GCC	1104
Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala	
355 360 365	
AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG GGG	1152
Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly	
370 375 380	
GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG GTC	1200
Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val	
385 390 395 400	
CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC TGC	1248
Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys	
405 410 415	
CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG AGG	1296
His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg	
420 425 430	
GCA CAG TCT GAG TCT GCC CGG AGC AAG	1323
Ala Gln Ser Glu Ser Ala Arg Ser Lys	
435 440	

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGG CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC	48
Arg Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala	
1 5 10 15	
CTC AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA	96
Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro	
20 25 30	
GCC AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG	144
Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val	
35 40 45	
GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG	192
Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln	
50 55 60	
GTC CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC	240
Val Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr	
65 70 75 80	
TGC CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG	288
Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp	
85 90 95	

AGG GCA CAG TCT GAG TCT GCC CGG AGC AAG  
 Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys  
 100 105

318

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1341

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG	48
Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu	
1 5 10 15	
TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA	96
Tyr Gly Thr Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
20 25 30	
GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC	144
Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly	
35 40 45	
GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA	192
Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg	
50 55 60	
TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC	240
Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly	
65 70 75 80	

GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr	85	90	95	288
AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys	100	105	110	336
AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly	115	120	125	384
TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly	130	135	140	432
ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu	145	150	155	480
TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr	165	170	175	528
GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln	180	185	190	576
GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu	195	200	205	624
ACT AAG AGG TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala	210	215	220	672
ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu	225	230	235	720
ATC TGC TTT GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp	245	250	255	768
CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC				816

Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe	
260 265 270	
CTC GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC	864
Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe	
275 280 285	
ATC CCT TCT GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC	912
Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly	
290 295 300	
CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC	960
Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro	
305 310 315 320	
ATG TCA GAG CTG ACA GAG ACT GGC GGA GGT GGC TCA GGC GGA GGT GGA	1008
Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly	
325 330 335	
TCT GGA GGT GGA GGC TCA CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC	1056
Ser Gly Gly Gly Gly Ser Arg Leu Glu Gln Pro Asn Val Ala Ile Ser	
340 345 350	
CTG TCC AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG	1104
Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser	
355 360 365	
GTG ACA GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT	1152
Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn	
370 375 380	
GGC CAG GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT	1200
Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn	
385 390 395 400	
GGG GAC TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT	1248
Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His	
405 410 415	
CAG GGA GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC	1296
Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser	
420 425 430	



CCC ATC ACT GTG GAG TGG AGG GCA CAG TCC GAG TCT GCC CGG AGC AAG  
 Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys  
 435 440 445

1341

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT	48
Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val	
1 5 10 15	
TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT	96
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	
GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG	144
Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg	
35 40 45	
CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu	
50 55 60	
CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	

TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC	288
Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe	
85 90 95	
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT	336
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe	
100 105 110	
GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT	384
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn	
115 120 125	
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC	432
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn	
130 135 140	
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT	480
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser	
145 150 155 160	
GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG	528
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu	
165 170 175	
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG	576
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu	
180 185 190	
CTG ACA GAG ACT	588
Leu Thr Glu Thr	
195	

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..312

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC AGG ACA GAG GCC	48
Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala	
1 5 10 15	
CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA GAT TTC TAC CCA	96
Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro	
20 25 30	
GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG GAG GAG ACA GTG	144
Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val	
35 40 45	
GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG	192
Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln	
50 55 60	
GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA GAG GTC TAC ACC	240
Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr	
65 70 75 80	
TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG	288
Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp	
85 90 95	
AGG GCA CAG TCC GAG TCT GCC CGG	312
Arg Ala Gln Ser Glu Ser Ala Arg	
100 105	

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp ~~Asp~~  
1 5 10 15